



BLASTP 2.2.10 [Oct-19-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1108406271-19060-109558541338.BLASTQ4

Query=

(226 letters)

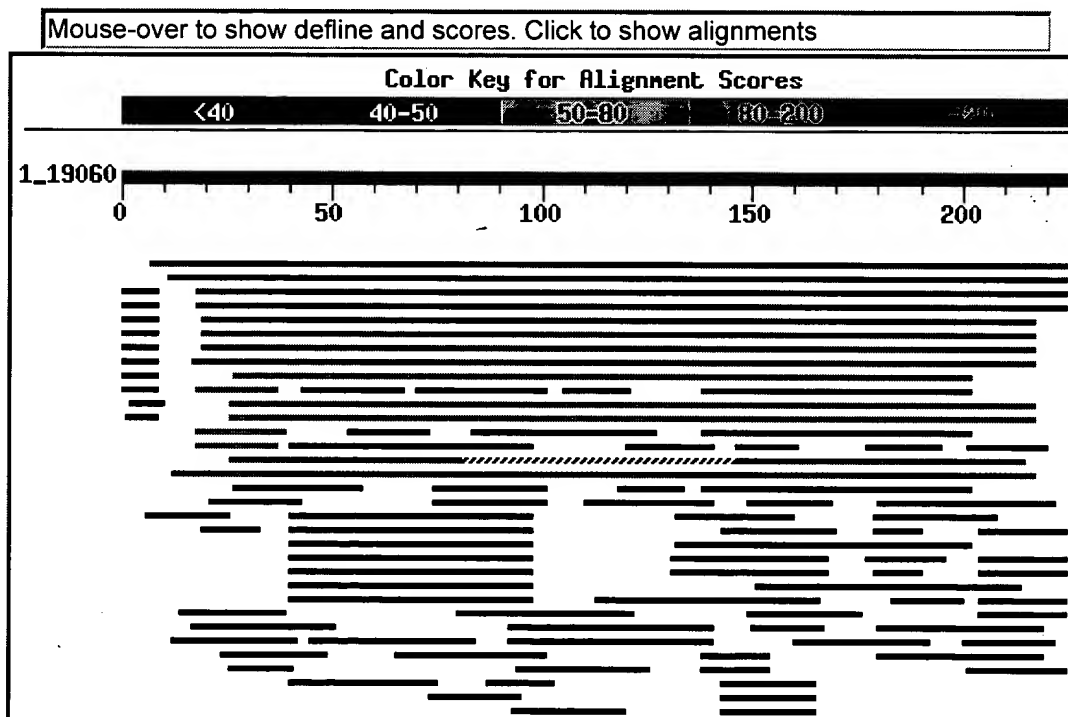
Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding environmental samples
2,326,143 sequences; 788,882,796 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 101 Blast Hits on the Query Sequence



[Related Structures](#)

Sequences producing significant alignments:		Score (bits)	E Value	
gi 505281 emb CAA41768.1 	exoenzyme C3 [Clostridium botulin...	630	e-179	
gi 747707 emb CAA35828.1 	exoenzyme C3 [Clostridium botulin...	627	e-178	
gi 51247865 pdb 1UZI B	Chain B, C3 Exoenzyme From Clostridi...	609	e-173	S
gi 23200102 pdb 1GZE D	Chain D, Structure Of The Clostridiu...	599	e-170	S
gi 399048 sp Q00901 ARC3_CBCP	Mono-ADP-ribosyltransferase C...	338	2e-91	
gi 56965901 pdb 1R4B B	Chain B, Adp-Ribosyltransferase C3bo...	338	2e-91	S
gi 404821 dbj BAA04492.1 	ADP-ribosyltransferase C3 [Clostr...	328	1e-88	
gi 1212875 emb CAA60674.1 	exoenzyme C3 [Clostridium limosu...	316	7e-85	
gi 22795813 emb CAD22164.1 	ADP-ribosyltransferase [Bacillu...	77	1e-12	
gi 236587 gb AAB19984.1 	ADP-ribosyltransferase exoenzyme C...	70	1e-10	
gi 13186140 emb CAC33493.1 	ADP-ribosyltransferase [Staphyl...	67	1e-09	S
gi 24636605 dbj BAC22946.1 	epidermal cell differentiation ...	67	1e-09	
gi 80491 pir S05236	exoenzyme C3 - Clostridium botulinum (...)	62	4e-08	
gi 236588 gb AAB19985.1 	ADP-ribosyltransferase exoenzyme C...	60	2e-07	
gi 17227179 ref NP_478345.1 	hypothetical protein [Staphylo...	59	2e-07	
gi 79857 pir JG0016	epidermal cell differentiation inhibit...	53	1e-05	
gi 249591 gb AAB22208.1 	ADP-ribosyltransferase [Clostridiu...	41	0.089	
gi 249592 gb AAB22209.1 	ADP-ribosyltransferase [Clostridiu...	40	0.12	
gi 6730536 pdb 1QS1 D	Chain D, Crystal Structure Of Vegetat...	40	0.12	S
gi 6730537 pdb 1QS2 A	Chain A, Crystal Structure Of Vip2 Wi...	40	0.12	S
gi 29650779 gb AAO86513.1 	Vip2Ac [Bacillus thuringiensis]	40	0.16	
gi 435823 gb AAB28629.1 	C3-like ADP-ribosyltransferase {NA...	38	0.39	
gi 45219853 gb AAH66784.1 	Autoantigen La [Xenopus tropical...	38	0.52	G
gi 29374726 ref NP_813878.1 	lipoprotein, putative [Enteroc...	35	3.0	G
gi 15893630 ref NP_346979.1 	Mono-ADP-ribosyltransferase C3...	35	3.0	G
gi 21315078 gb AAH30775.1 	ARTS-1 protein [Homo sapiens] >g...	35	4.0	G
gi 37182302 gb AAQ88953.1 	ARTS-1 [Homo sapiens]	35	4.0	G
gi 6642987 gb AAF20384.1 	aminopeptidase PILS [Homo sapiens]	35	4.0	G
gi 6381989 gb AAF07395.1 	adipocyte-derived leucine aminope...	35	4.0	G
gi 19879276 gb AAK37778.1 	adipocyte-derived leucine aminop...	35	4.0	G
gi 23509168 ref NP_701836.1 	hypothetical protein PFL2380c ...	35	4.0	G
gi 55625752 ref XP_527213.1 	PREDICTED: similar to adipocyt...	35	4.0	G
gi 20137531 sp Q9NZ08 ART1_HUMAN	Adipocyte-derived leucine ...	35	4.0	G
gi 20521069 dbj BAA25451.2 	KIAA0525 protein [Homo sapiens]	35	4.0	G
gi 29655312 ref NP_821004.1 	adenosylhomocysteinase [Coxiel...	35	5.4	G
gi 64876 emb CAA48716.1 	La protein form B [Xenopus laevis]...	34	7.3	G
gi 28436825 gb AAH46654.1 	MGC52876 protein [Xenopus laevis]	34	7.3	G
gi 50083934 ref YP_045444.1 	hypothetical protein; putative...	34	7.3	G
gi 2344808 emb CAB05387.1 	unknown [Helicobacter pylori]	34	7.3	
gi 18144707 dbj BAB80752.1 	hypothetical protein [Clostridi...	34	7.3	G
gi 1006663 emb CAA84542.1 	MDR3 P-glycoprotein [Homo sapiens]	34	9.8	G
gi 51473693 ref YP_067450.1 	rickettsial conserved hypothet...	34	9.8	G
gi 48847109 ref ZP_00301367.1 	COG0443: Molecular chaperone...	34	9.8	
gi 48844634 ref ZP_00298937.1 	hypothetical protein Gmet020...	34	9.8	
gi 48844300 ref ZP_00298619.1 	COG0525: Valyl-tRNA syntheta...	34	9.8	
gi 48844054 ref ZP_00298396.1 	COG2025: Electron transfer f...	34	9.8	
gi 48843994 ref ZP_00298350.1 	hypothetical protein Gmet020...	34	9.8	
gi 34764189 ref ZP_00145051.1 	TYPE I RESTRICTION-MODIFICAT...	34	9.8	

gi 2313683 gb AAD07632.1	H. pylori predicted coding region...	34	9.8	G
gi 41723241 ref ZP_00150184.1	COG0642: Signal transduction...	34	9.8	
gi 39594284 emb CAE71862.1	Hypothetical protein CBG18908 [...]	34	9.8	
gi 39583135 emb CAE60675.1	Hypothetical protein CBG04328 [...]	34	9.8	
gi 14276022 dbj BAB58942.1	phenol hydroxylase large subuni...	34	9.8	
gi 730030 sp P40631 MLH_TETTH	Micronuclear linker histone p...	33	13	
gi 57208133 emb CAI40768.1	Isp2a protein [Brevibacillus la...	33	13	
gi 51556700 ref YP_068061.1	pTP [Tree shrew adenovirus]	33	13	G
gi 27468972 ref NP_765609.1	hypothetical protein SE2054 [S...	33	18	G
gi 57865475 ref YP_189623.1	membrane protein, putative [St...	33	18	G
gi 53687109 ref ZP_00107385.2	COG1177: ABC-type spermidine...	33	18	
gi 51013377 gb AAT92982.1	YHR005C [Saccharomyces cerevisia...	32	24	G
gi 173560 gb AAA18403.1	putative. G-alpha-like protein	32	24	
gi 24377635 gb AAN58940.1	conserved hypothetical protein; ...	32	24	G
gi 7511574 pir T18747	probable potassium channel protein -...	32	24	
gi 48733274 ref ZP_00267017.1	COG3451: Type IV secretory p...	32	32	
gi 30022154 ref NP_833785.1	Stage V sporulation protein AD...	32	32	G
gi 47529582 ref YP_020931.1	stage v sporulation protein ad...	32	32	G
gi 50906527 ref XP_464752.1	putative pentatricopeptide (PP...	32	32	G
gi 52141425 ref YP_085404.1	stage V sporulation protein AD...	32	32	G
gi 42783182 ref NP_980429.1	stage V sporulation protein AD...	32	32	G
gi 48870644 ref ZP_00323364.1	COG3010: Putative N-acetylma...	32	32	
gi 48854717 ref ZP_00308878.1	COG5651: PPE-repeat proteins...	32	32	
gi 47565952 ref ZP_00236991.1	stage V sporulation protein ...	32	32	
gi 53687444 ref ZP_00108980.2	COG4644: Transposase and ina...	32	32	
gi 39587376 emb CAE75030.1	Hypothetical protein CBG22937 [...]	32	32	
gi 454862 gb AAA69970.1	region near C-terminus; putative	32	32	
gi 16081318 ref NP_393636.1	hypothetical protein Ta0158 [T...	32	43	G
gi 54641100 gb EAL29851.1	GA20157-PA [Drosophila pseudoobs...	32	43	
gi 52352362 gb AAU43652.1	FAD/FMN-containing dehydrogenase...	32	43	
gi 15828932 ref NP_326292.1	hypothetical protein MYPU_4610...	31	57	G
gi 34104158 gb AAQ60517.1	conserved hypothetical protein [...]	31	57	G
gi 27467268 ref NP_763905.1	penicillin amidase V [Staphylo...	31	57	G
gi 49474859 ref YP_032900.1	Adenosylhomocysteinase [Barton...	31	57	G
gi 57168708 ref ZP_00367840.1	conserved hypothetical prote...	31	57	
gi 41409460 ref NP_962296.1	SahH [Mycobacterium avium subs...	31	57	G
gi 29653858 ref NP_819550.1	excinuclease ABC, B subunit [C...	31	57	G
gi 52549567 gb AAU83416.1	FAD FMN containing dehydrogenase...	31	57	
gi 30025120 gb AAC69093.2	Innexin protein 5 [Caenorhabditi...	31	57	
gi 28828803 gb AAO51398.1	hypothetical protein [Dictyostel...	31	57	
gi 50308841 ref XP_454425.1	unnamed protein product [Kluyv...	31	57	G
gi 48097538 ref XP_391917.1	similar to CG11654-PA [Apis me...	31	57	G
gi 57866161 ref YP_187823.1	penicillin V acylase, putative...	31	57	G
gi 17568579 ref NP_509403.1	innexin, putative gap junction...	31	57	G
gi 53735789 ref ZP_00178447.2	hypothetical protein Cwat030...	31	57	
gi 46143226 ref ZP_00135639.2	COG1404: Subtilisin-like ser...	31	57	
gi 39583806 emb CAE74879.1	Hypothetical protein CBG22739 [...]	31	57	
gi 38491955 gb AAR22310.1	mitochondrial intermediate pepti...	31	57	
gi 51534847 dbj BAD37204.1	nitrite reductase [uncultured b...	31	57	
gi 236586 gb AAB19983.1	ADP-ribosyltransferase exoenzyme C...	31	57	
gi 54020612 ref YP_116107.1	DNA polymerase III alpha chain...	31	77	G
gi 53729791 ref ZP_00150191.2	COG2887: RecB family exonucl...	31	77	

Alignments

Get selected sequences

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Deselect all

☐ >gi|505281|emb|CAA41768.1| exoenzyme C3 [Clostridium botulinum D phage]
 gi|296787|emb|CAA41767.1| exoenzyme C3 [Clostridium botulinum C phage]
 gi|625586|pir||A38912 NAD+-asparagine ADP-ribosyltransferase (EC 2.4.2.-) C3 prec
 Clostridium botulinum phage (strain CST)
 gi|399049|sp|P15879|ARC3_CBDP Mono-ADP-ribosyltransferase C3 precursor (Exoenzyme
 Length = 251

Score = 630 bits (1479), Expect = e-179

Identities = 209/224 (93%), Positives = 210/224 (93%), Gaps = 7/224 (3%)

Query: 8 QACNAYSFNQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGK 67
 Q C AYS NQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGK
 Sbjct: 30 QKCYAYSINQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGK 89

Query: 68 LRQNKGVINGFPSNLIQ--WLLDKSFNKMKT PENIMLFXGDDPAYLGTEFQNTLLNSNG 125
 LRQNKGVINGFPSNLIQ LLDKSFNKMKT PENIMLFXGDDPAYLGTEFQNTLLNSNG
 Sbjct: 90 LRQNKGVINGFPSNLIQVE-LLDKSFNKMKT PENIMLFRGDDPAYLGTEFQNTLLNSNG 148

Query: 126 TINKTAFEKAKAIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPIS 185
 TINKTAFEKAKA +FLN DRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPIS
 Sbjct: 149 TINKTAFEKAKA-KFLNKDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPIS 207

Query: 186 AFQGGLEG-LPRHSTYHIDDMRLSSDGKQIIITAT--GTAINPK 226
 AF GQLE LPRHSTYHIDDMRLSSDGKQIIITAT GTAINPK
 Sbjct: 208 AFAGQLEMLLPRHSTYHIDDMRLSSDGKQIIITATMMGTAINPK 251

☐ >gi|747707|emb|CAA35828.1| exoenzyme C3 [Clostridium botulinum D phage]
 Length = 218

Score = 627 bits (1472), Expect = e-178

Identities = 207/220 (94%), Positives = 208/220 (94%), Gaps = 7/220 (3%)

Query: 12 AYSFNQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQN 71
 AYS NQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQN
 Sbjct: 1 AYSINQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQN 60

Query: 72 KGVINGFPSNLIQ--WLLDKSFNKMKT PENIMLFXGDDPAYLGTEFQNTLLNSNGTINK 129
 KGVINGFPSNLIQ LLDKSFNKMKT PENIMLFXGDDPAYLGTEFQNTLLNSNGTINK
 Sbjct: 61 KGVINGFPSNLIQVE-LLDKSFNKMKT PENIMLFRGDDPAYLGTEFQNTLLNSNGTINK 119

Query: 130 TAFEKAKAIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQG 189
 TAFEKAKA +FLN DRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAF G
 Sbjct: 120 TAFEKAKA-KFLNKDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFAG 178

Query: 190 QLEG-LPRHSTYHIDDMRLSSDGKQIIITAT--GTAINPK 226
 QLE LPRHSTYHIDDMRLSSDGKQIIITAT GTAINPK
 Sbjct: 179 QLEMLLPRHSTYHIDDMRLSSDGKQIIITATMMGTAINPK 218

☐ >gi|51247865|pdb|1UZI|B **S** Chain B, C3 Exoenzyme From Clostridium Botulinum, Tetr
 gi|51247864|pdb|1UZI|A **S** Chain A, C3 Exoenzyme From Clostridium Botulinum, Tetrag
 gi|23200106|pdb|1GZF|D **S** Chain D, Structure Of The Clostridium Botulinum C3 Exoen
 (Wild-Type) In Complex With Nad
 gi|23200105|pdb|1GZF|C **S** Chain C, Structure Of The Clostridium Botulinum C3 Exoen
 (Wild-Type) In Complex With Nad
 gi|23200104|pdb|1GZF|B **S** Chain B, Structure Of The Clostridium Botulinum C3 Exoen
 (Wild-Type) In Complex With Nad
 gi|23200103|pdb|1GZF|A **S** Chain A, Structure Of The Clostridium Botulinum C3 Exoen
 (Wild-Type) In Complex With Nad
 gi|12084428|pdb|1G24|D **S** Chain D, The Crystal Structure Of Exoenzyme C3 From Clos
 Botulinum
 gi|12084427|pdb|1G24|C **S** Chain C, The Crystal Structure Of Exoenzyme C3 From Clos
 Botulinum
 gi|12084426|pdb|1G24|B **S** Chain B, The Crystal Structure Of Exoenzyme C3 From Clos
 Botulinum
 gi|12084425|pdb|1G24|A **S** Chain A, The Crystal Structure Of Exoenzyme C3 From Clos
 Botulinum
 Length = 211

Score = 609 bits (1429), Expect = e-173

Identities = 201/213 (94%), Positives = 202/213 (94%), Gaps = 7/213 (3%)

Query: 19 AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF 78
 AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF

Sbjct: 1 AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF 60

Query: 79 PSNLIKQ--WLLDKSFNKMKTPENIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFEKAK 136
 PSNLIKQ LLDKSFNKMKTPENIMLF GDDPAYLGTEFQNTLLNSNGTINKTAFEKAK

Sbjct: 61 PSNLIKQVE-LLDKSFNKMKTPENIMLFRGDDPAYLGTEFQNTLLNSNGTINKTAFEKAK 119

Query: 137 AIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQGOLEG-LP 195
 A +FLN DRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAF GQLE LP

Sbjct: 120 A-KFLNKDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFAGQLEMLLP 178

Query: 196 RHSTYHIDDMRLSSDGKQIIITAT--GTAINPK 226
 RHSTYHIDDMRLSSDGKQIIITAT GTAINPK

Sbjct: 179 RHSTYHIDDMRLSSDGKQIIITATMMGTAINPK 211

☐ >gi|23200102|pdb|1GZE|D **S** Chain D, Structure Of The Clostridium Botulinum C3 Exo
 Mutant)
 gi|23200101|pdb|1GZE|C **S** Chain C, Structure Of The Clostridium Botulinum C3 Exoen
 Mutant)
 gi|23200100|pdb|1GZE|B **S** Chain B, Structure Of The Clostridium Botulinum C3 Exoen
 Mutant)
 gi|23200099|pdb|1GZE|A **S** Chain A, Structure Of The Clostridium Botulinum C3 Exoen
 Mutant)
 Length = 211

Score = 599 bits (1407), Expect = e-170

Identities = 200/213 (93%), Positives = 201/213 (94%), Gaps = 7/213 (3%)

Query: 19 AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF 78
 AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF
 Sbjct: 1 AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF 60

Query: 79 PSNLIQ--WLLDKSFNKMKTPEINIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFEKAK 136
 PSNLIQ LLDKSFNKMKTPEINIMLF GDDPAYLGTEFQNTLLNSNGTINKTAFEKAK
 Sbjct: 61 PSNLIQVE-LLDKSFNKMKTPEINIMLFRGDDPAYLGTEFQNTLLNSNGTINKTAFEKAK 119

Query: 137 AIQFLNXDRLEYGYISTSMLNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQGQLEG-LP 195
 A +FLN DRLEYGYISTS MNVSQFAGRPIITKFKVAKGSKAGYIDPISAF GQLE LP
 Sbjct: 120 A-KFLNKDRLEYGYISTSMLNVSQFAGRPIITKFKVAKGSKAGYIDPISAFAGQLEMLLP 178

Query: 196 RHSTYHIDDMRLSSDGKQIIITAT--GTAINPK 226
 RHSTYHIDDMRLSSDGKQIIITAT GTAINPK
 Sbjct: 179 RHSTYHIDDMRLSSDGKQIIITATMMGTAINPK 211

☐ >gi|399048|sp|Q00901|ARC3_CBCP Mono-ADP-ribosyltransferase C3 precursor (Exoenzy
 gi|80492|pir||A41021 NAD+-asparagine ADP-ribosyltransferase (EC 2.4.2.-) C3 precu
 Clostridium botulinum phage (strain C003-9)
 gi|144737|gb|AAA23212.1| C3 ADP-ribosyltransferase
 Length = 244

Score = 338 bits (791), Expect = 2e-91

Identities = 129/205 (62%), Positives = 163/205 (79%), Gaps = 12/205 (5%)

Query: 20 YSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFP 79
 Y++T+ EFTN+++AK WGNAQYKKYGLSK E+EAI YT+ AS+ING LR N+G NG P
 Sbjct: 42 YADTFTEFTNVEEAKKWGNAQYKKYGLSKPEQEAIKFYTRDASKINGPLRANQGNENGLP 101

Query: 80 SNL---IKQWLLDKSFNKMKTPEINIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFE--K 134
 +++ +K L+D+SF+KMK P+NI+LF GDDPAYLG EFQ+ +LN +GTINKT FE K
 Sbjct: 102 ADILQKVK--LIDQSFSKMKMPQNIILFRGDDPAYLGPEFQDKILNKDGTINKTVFEQVK 159

Query: 135 AKAIQFLNXDRLEYGYISTSMLNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQGQLEG- 193
 AK FL DR EYGYISTSML+ +QF GRPI+TKFKV GSK GYIDPIS F GQLE
 Sbjct: 160 AK---FLKKDRTEYGYISTSMLS-AQFGGRPIVTKFKVTNGSKGGYIDPISYFPGQLEVL 215

Query: 194 LPRHSTYHIDDMRLSSDGKQIIITA 218
 LPR+++Y+I DM++S + +QI+ITA
 Sbjct: 216 LPRNNSYYISDMQISPNNRQIMITA 240

☐ >gi|56965901|pdb|1R4B|B **S** Chain B, Adp-Ribosyltransferase C3bot2 From Clostridiu
 Monoclinic Form

gi|56965900|pdb|1R4B|A **S** Chain A, Adp-Ribosyltransferase C3bot2 From Clostridium
 Monoclinic Form

gi|56965899|pdb|1R45|D **S** Chain D, Adp-Ribosyltransferase C3bot2 From Clostridium
 Triclinic Form

gi|56965898|pdb|1R45|C **S** Chain C, Adp-Ribosyltransferase C3bot2 From Clostridium
 Triclinic Form

gi|56965897|pdb|1R45|B **S** Chain B, Adp-Ribosyltransferase C3bot2 From Clostridium
 Triclinic Form

gi|56965896|pdb|1R45|A **S** Chain A, Adp-Ribosyltransferase C3bot2 From Clostridium
 Triclinic Form
 Length = 204

Score = 338 bits (791), Expect = 2e-91
Identities = 129/205 (62%), Positives = 163/205 (79%), Gaps = 12/205 (5%)

Query: 20 YSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFP 79
Y++T+ EFTN+++AK WGNAQYKKYGLSK E+EAI YT+ AS+ING LR N+G NG P
Sbjct: 2 YADTFTEFTNVEEAKKWGNAQYKKYGLSKPEQEAIKFYTRDASKINGPLRANQGNENGLP 61

Query: 80 SNL---IKQWLLDKSFNKMKTPEINIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFE--K 134
+++ +K L+D+SF+KMK P+NI+LF GDDPAYLG EFQ+ +LN +GTINKT FE K
Sbjct: 62 ADILQKVK--LIDQSFSSKMKMPQNIILFRGDDPAYLGPEFQDKILNKDGTINKTVFEQVK 119

Query: 135 AKAIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQGQLEG- 193
AK FL DR EYGYISTSLM+ +QF GRPI+TKFKV GSK GYIDPIS F GQLE
Sbjct: 120 AK---FLKKDRTEYGYISTSLMS-AQFGGRPIVTKFKVTNGSKGGYIDPISYFPQGQLEVL 175

Query: 194 LPRHSTYHIDDMRLSSDGKQIIITA 218
LPR+++Y+I DM++S + +QI+ITA
Sbjct: 176 LPRNNSYYISDMQISPNNRQIMITA 200

☐ >gi|404821|dbj|BAA04492.1| ADP-ribosyltransferase C3 [Clostridium botulinum D]
Length = 244

Score = 328 bits (768), Expect = 1e-88
Identities = 127/205 (61%), Positives = 161/205 (78%), Gaps = 12/205 (5%)

Query: 20 YSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFP 79
Y++T+ EFTN+++AK WGNAQYKKYGLSK E+EAI YT+ AS+ING LR N+G NG
Sbjct: 42 YADTFTEFTNVEEAKKWGNAQYKKYGLSKPEQEAIKFYTRDASKINGPLRANQGNENGLS 101

Query: 80 SNL---IKQWLLDKSFNKMKTPEINIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFE--K 134
S++ +K L+D+SF+KMK P+NI+LF GDDPAYLG EFQ+ +LN +GTIN+ FE K
Sbjct: 102 SDILQKVK--LIDQSFSSKMKMPQNIILFRGDDPAYLGPEFQDKILNKDGTINRDVFEQVK 159

Query: 135 AKAIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQGQLEG- 193
AK FL DR EYGYISTSLM+ +QF GRPI+TKFKV GSK GYIDPIS F GQLE
Sbjct: 160 AK---FLKKDRTEYGYISTSLMS-AQFGGRPIVTKFKVTNGSKGGYIDPISYFPQGQLEVL 215

Query: 194 LPRHSTYHIDDMRLSSDGKQIIITA 218
LPR+++Y+I DM++S + +QI+ITA
Sbjct: 216 LPRNNSYYISDMQISPNNRQIMITA 240

☐ >gi|1212875|emb|CAA60674.1| exoenzyme C3 [Clostridium limosum]
gi|2498151|sp|Q46134|ARC3 CLOLM Mono-ADP-ribosyltransferase C3 precursor (Exoenzy
gi|11282305|pir||A46957 NAD+-asparagine ADP-ribosyltransferase (EC 2.4.2.-) C3-li
precursor [validated] - Clostridium limosum phage
Length = 250

Score = 316 bits (739), Expect = 7e-85
Identities = 126/205 (61%), Positives = 160/205 (78%), Gaps = 7/205 (3%)

Query: 18 KAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVING 77
K Y++++EFTNID+A+AWG+ Q+ KY LS SEK A+ YT++A+ ING LR N+G NG
Sbjct: 45 KPYADSFKEFTNIDEARAWGDKQFAKYKLSSEKNALTIYTRNAARINGPLRANQGNTNG 104

Query: 78 FPSNLIK---QWLLDKSFNKMKTPEINIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFEK 134
P+++ K Q +DKSF KM+TPENI+LF GDDP YLG +F+NT+LN +GTINK FE+
Sbjct: 105 LPADIRKEVEQ--IDKSFTKMQTPEINILFRGDDPGYLGPDFENTILNRDGTINKAVFEQ 162

Query: 135 AKAIQFLNXDRLEYGYISTSLMNVSQFAGRPITKFKVAKGSKAGYIDPISAFQGGLEG- 193
K ++F DR EYGYISTSL+N S FAGRPITKFKV GSKAGYI+PIS F+GQLE
Sbjct: 163 VK-LRFKKGDRKEYGYISTSLVNGSAFAGRPITKFKVLDGSKAGYIEPISTFKGQLEVL 221

Query: 194 LPRHSTYHIDDMRLSSDGKQIIITA 218
LPR STY I DM+++ + KQIIITA
Sbjct: 222 LPRSSTYTISDMQIAPNNKQIIITA 246

☐ >[gi|22795813|emb|CAD22164.1|](#) ADP-ribosyltransferase [Bacillus cereus]
Length = 219

Score = 76.6 bits (173), Expect = 1e-12
Identities = 74/209 (35%), Positives = 108/209 (51%), Gaps = 64/209 (30%)

Query: 28 TNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEIN-----GKL-----RQNKGVI 75
TN ++A AWG Q+ K+ SK EK AI YTK+A N GKL + K I
Sbjct: 20 TNKEEADAWGKKQFNKW--SKEEKSAIRDYTKNARPYNEFLRMHAGKLDSDPTMKKK--I 75

Query: 76 NGFPSNLIKQWLLDKSFNKM--KTPENIMLFXGDDPAYL-GTEFQNTLLNSNGTINKTAF 132
LDK+ N+ K +NI ++ GDD A++ G E+ N+++ NG +++
Sbjct: 76 ES-----LDKALNRKEAKVNDNIKVYRGDD-AWIFGKEYDNSIIK-NGKVDR--- 120

Query: 133 EKAKAIQ--FLNXDRL-----EYGYISTS-LMNVSQFAG----RPIITKFKVAKGSKAG 179
EK K IQ F E+GYISTS L++ AG RP++T+FKV G+
Sbjct: 121 EKFKIEIKKKF-----QGKTTTEFGYISTSILID----AGYAKTRPVMTEFKVGSNGTHA 170

Query: 180 YI--DPISAFQGG---LEGLPRHSTYHID 203
Y+ D ++A+ GQ L LPR++ Y I+
Sbjct: 171 YMNSDDLTAYPGQYELL--LPRNTVYKIE 197

☐ >[gi|236587|gb|AAB19984.1|](#) ADP-ribosyltransferase exoenzyme C3 [Clostridium botul
C strain Stockholm, CST, Peptide Partial, 20 aa]
Length = 20

Score = 69.8 bits (157), Expect = 1e-10
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 19 AYSNTYQEFTNIDQAKAWGN 38
AYSNTYQEFTNIDQAKAWGN
Sbjct: 1 AYSNTYQEFTNIDQAKAWGN 20

☐ >[gi|13186140|emb|CAC33493.1|](#) ADP-ribosyltransferase [Staphylococcus aureus]
[gi|34810145|pdb|1OJZ|A](#) ☒ Chain A, The Crystal Structure Of C3stau2 From S. Aureus
Nad
[gi|34810144|pdb|1OJQ|A](#) ☒ Chain A, The Crystal Structure Of C3stau2 From S. Aureus
Length = 212

Score = 66.8 bits (150), Expect = 1e-09

Identities = 78/232 (33%), Positives = 113/232 (48%), Gaps = 70/232 (30%)

Query: 27 FTNIDQAKAWGNAQYK--KYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFPSNL-- 82
 FT++ +A WGN+ K KY SK +K AI +YTK++S IN LR G +N N+
 Sbjct: 6 FTDLVEATKWGNSLIKSAKYS-SK-DKMAIYNYTKNSSPINTPLRSANGDVNKLSENIQE 63

Query: 83 -IKQWLLDKSFNKMKTPENI----MLFXGDDPAYLG--TEF-----Q----- 117
 ++Q LD + +K TP+++ +L + YL T F Q
 Sbjct: 64 QVRQ--LDSTISKSVTPDSVYVYRLL----NLDYLSSITGFTREDLHMLQQTNNNGQYNEA 117

Query: 118 -----NTLLNSNGTINKTAFEKAKAIQFLNXDRL--EYGYISTSLMNVSQFAGRPIITKF 170
 N L+NS R+ E GY ST L++ + AGRPI K
 Sbjct: 118 LVSKLNNLMNS-----RIYRENGYSSTQLVSGAALAGRPIELKL 156

Query: 171 KVAKGSKAGYIDP--ISAFQGQLEG-LPRHSTYHIDDMRLSSDGKQ-IIITA 218
 ++ KG+KA YID ++A+ GQ E LPR + Y + ++L SD K+ IIITA
 Sbjct: 157 ELPKGTAKAAYIDSKELTAYPGQQEVLLPRGTEYAVGSVKL-SDNKRKIIITA 207

☐ >gi|24636605|dbj|BAC22946.1| epidermal cell differentiation inhibitor B [Staphyl
 Length = 247

Score = 66.8 bits (150), Expect = 1e-09

Identities = 78/232 (33%), Positives = 113/232 (48%), Gaps = 70/232 (30%)

Query: 27 FTNIDQAKAWGNAQYK--KYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFPSNL-- 82
 FT++ +A WGN+ K KY SK +K AI +YTK++S IN LR G +N N+
 Sbjct: 41 FTDLVEATKWGNSLIKSAKYS-SK-DKMAIYNYTKNSSPINTPLRSANGDVNKLSENIQE 98

Query: 83 -IKQWLLDKSFNKMKTPENI----MLFXGDDPAYLG--TEF-----Q----- 117
 ++Q LD + +K TP+++ +L + YL T F Q
 Sbjct: 99 QVRQ--LDSTISKSVTPDSVYVYRLL----NLDYLSSITGFTREDLHMLQQTNNNGQYDEA 152

Query: 118 -----NTLLNSNGTINKTAFEKAKAIQFLNXDRL--EYGYISTSLMNVSQFAGRPIITKF 170
 N L+NS R+ E GY ST L++ + AGRPI K
 Sbjct: 153 LVSKLNNLMNS-----RIYRENGYSSTQLVSGAALAGRPIELKL 191

Query: 171 KVAKGSKAGYIDP--ISAFQGQLEG-LPRHSTYHIDDMRLSSDGKQ-IIITA 218
 ++ KG+KA YID ++A+ GQ E LPR + Y + ++L SD K+ IIITA
 Sbjct: 192 ELPKGTAKAAYIDSKELTAYPGQQEVLLPRGTEYAVGSVKL-SDNKRKIIITA 242

☐ >gi|80491|pir||S05236 exoenzyme C3 - Clostridium botulinum (fragment)
 Length = 22

Score = 61.7 bits (138), Expect = 4e-08

Identities = 21/23 (91%), Positives = 21/23 (91%), Gaps = 2/23 (8%)

Query: 19 AYSNTYQEF-TNIDQAKAWGNAQ 40
 AYSNTYQEF TNIDQAKA GNAQ
 Sbjct: 1 AYSNTYQEFNTNIDQAKA-GNAQ 22

☐ >gi|236588|gb|AAB19985.1| ADP-ribosyltransferase exoenzyme C3 [Clostridium botul
 D strain D1873, Peptide Partial, 20 aa]
 Length = 20

Score = 59.6 bits (133), Expect = 2e-07
Identities = 19/20 (95%), Positives = 19/20 (95%)

Query: 19 AYSNTYQEFTNIDQAKAWGN 38
AYSNTYQEFTNIDQAKA GN
Sbjct: 1 AYSNTYQEFTNIDQAKAXGN 20

☐ >gi|17227179|ref|NP_478345.1| hypothetical protein [Staphylococcus aureus]
gi|17148579|dbj|BAB78400.1| ORF2~epidermal cell differentiation inhibitor C of St
aureus
Length = 247

Score = 59.2 bits (132), Expect = 2e-07
Identities = 35/75 (46%), Positives = 49/75 (65%), Gaps = 7/75 (9%)

Query: 147 EYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDP--ISAFQGG---LEGLPRHSTYH 201
EYGY ST L+ + AGRPI K ++ KG+KA YID ++A+ GQ L LPR + Y
Sbjct: 168 EYGYSSSTQLVKGAALAGRPIELKLQLPKGTAAAYIDSKNLTAYPGQQEIL--LPRGTDYT 225

Query: 202 IDDMRLSSDGKQIII 216
I+ ++LS D K+I+I
Sbjct: 226 INTVKLSDDHKRILI 240

Score = 43.9 bits (96), Expect = 0.008
Identities = 26/61 (42%), Positives = 37/61 (60%), Gaps = 10/61 (16%)

Query: 27 FTNIDQAKAWGN-----AQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFPSN 81
FT++ +A WGN A Y SK +KEAI +YTK +S IN LR ++G I+ F ++
Sbjct: 41 FTDLTEATNWGNKLIKQANYS----SK-DKEAIYNYTKYSSPINTPLRSSQGDISNFSAD 95

Query: 82 L 82
L
Sbjct: 96 L 96

☐ >gi|79857|pir||JG0016 epidermal cell differentiation inhibitor precursor - Staph
aureus
gi|119131|sp|P24121|EDIN STAAU Epidermal cell differentiation inhibitor precursor
gi|152998|gb|AAA26616.1| epidermal cell differentiation inhibitor
Length = 247

Score = 53.2 bits (118), Expect = 1e-05
Identities = 89/261 (34%), Positives = 119/261 (45%), Gaps = 93/261 (35%)

Query: 13 YSFNQK--AYSNTY-----QEFTNIDQAKAWGNAQYK-----KYGLSKSEKEAIVSYTKS 60
YS N K SNT + FT++D+A WGN K KY S +K A+ YTK
Sbjct: 20 YSINDKIIEVSNTSLAADVKNFDTLDEATKWGN---KLIKQAKY--SSDDKIALYEYTKD 74

Query: 61 ASEINGKLRQNKGVINGFPSNLIKQWL-----LDKSFNKMKT PENI----ML--- 103
+S+ING LR G IN K L LD S +K TPE++ +L
Sbjct: 75 SSKINGPLRLAGGDIN-----K--LDSTTQDKVRRLDSSISKSTTPESVYVYRLLNLD 125

Query: 104 -----FXGDDPAY-LGTEFQNTLLNSNGTINKTAFEKAKAIQF-----LN---XDR 145